

10/560157

SEQUENCE LISTING

JAP13 Rec'd PCT/PTO 09 DEC 2005

<110> Pietrangelo, Antonello
<120> Mutations in the SLC40A1 gene associated to impaired iron homeostasis
<130> 8907-109-999
<140> To be Determined
<141> 2005-12-09
<150> PCT/EP2004/051068
<151> 2004-06-09
<160> 30
<170> PatentIn version 3.1
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<211> 1716
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> (1)..(1716)
<223> cDNA encoding wild type ferroportin 1. Polymorphisms related to the codons:
238-240 (G80), 520-522 (N174), 742-744 (Q248)

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Ser Leu Ser Thr Trp Gly Asp Arg Met Trp His Phe Ala Val Ser Val		
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Phe Leu Val Glu Leu Tyr Gly Asn Ser Leu Leu Leu Thr Ala Val Tyr		
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Gly Leu Val Val Ala Gly Ser Val Leu Val Leu Gly Ala Ile Ile Gly		
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gac tgg gtg gac aag aat gct aga ctt aaa gtg gcc cag acc tcg ctg		288
Asp Trp Val Asp Lys Asn Ala Arg Leu Lys Val Ala Gln Thr Ser Leu		
85 90 95		
gtg gta cag aat gtt tca gtc atc ctg tgt gga atc atc ctg atg atg		336
Val Val Gln Asn Val Ser Val Ile Leu Cys Gly Ile Ile Leu Met Met		
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gtt ttc tta cat aaa cat gag ctt ctg acc atg tac cat gga tgg gtt		384

Val Phe Leu His Lys His Glu Leu Leu Thr Met Tyr His Gly Trp Val			
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ctc act tcc tgc tat atc ctg atc atc act att gca aat att gca aat		432	
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ttg gcc agt act gct act gca atc aca atc caa agg gat tgg att gtt		480	
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Val Val Ala Gly Glu Asp Arg Ser Lys Leu Ala Asn Met Asn Ala Thr			
165	170	175	
ata cga agg att gac cag tta acc aac atc tta gcc ccc atg gct gtt		576	
Ile Arg Arg Ile Asp Gln Leu Thr Asn Ile Leu Ala Pro Met Ala Val			
180	185	190	
ggc cag att atg aca ttt ggc tcc cca gtc atc ggc tgt ggc ttt att		624	
Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys Gly Phe Ile			
195	200	205	
tcg gga tgg aac ttg gta tcc atg tgc gtg gag tac gtc ctg ctc tgg		672	
Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val Leu Leu Trp			
210	215	220	
aag gtt tac cag aaa acc cca gct cta gct gtg aaa gct ggt ctt aaa		720	
Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala Gly Leu Lys			
225	230	235	240
gaa gag gaa act gaa ttg aaa cag ctg aat tta cac aaa gat act gag		768	
Glu Glu Glu Thr Glu Leu Lys Gln Leu Asn Leu His Lys Asp Thr Glu			
245	250	255	
cca aaa ccc ctg gag gga act cat cta atg ggt gtg aaa gac tct aac		816	
Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys Asp Ser Asn			
260	265	270	
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Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala Ser Gln Met			
275	280	285	
gct gag ccc ttc cgt acc ttc cga gat gga tgg gtc tcc tac tac aac		912	
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Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu Tyr Met Thr			
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Val Leu Gly Phe Asp Cys Ile Thr Thr Gly Tyr Ala Tyr Thr Gln Gly			
325	330	335	
ctg agt ggt tcc atc ctc agt att ttg atg gga gca tca gct ata act		1056	
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Gly Ile Met Gly Thr Val Ala Phe Thr Trp Leu Arg Arg Lys Cys Gly			

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		380	
atc ttg tgt gtg atc tct gta ttc atg cct gga agc ccc ctg gac ttg Ile Leu Cys Val Ile Ser Val Phe Met Pro Gly Ser Pro Leu Asp Leu	385	390	1200
		395	400
tcc gtt tct cct ttt gaa gat atc cga tca agg ttc att caa gga gag Ser Val Ser Pro Phe Glu Asp Ile Arg Ser Arg Phe Ile Gln Gly Glu	405	410	1248
			415
tca att aca cct acc aag ata cct gaa att aca act gaa ata tac atg Ser Ile Thr Pro Thr Lys Ile Pro Glu Ile Thr Thr Glu Ile Tyr Met	420	425	1296
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tct aat ggg tct aat tct gct aat att gtc ccg gag aca agt cct gaa Ser Asn Gly Ser Asn Ser Ala Asn Ile Val Pro Glu Thr Ser Pro Glu	435	440	1344
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tct gtg ccc ata atc tct gtc agt ctg ctg ttt gca ggc gtc att gct Ser Val Pro Ile Ile Ser Val Ser Leu Leu Phe Ala Gly Val Ile Ala	450	455	1392
			460
gct aga atc ggt ctt tgg tcc ttt gat tta act gtg aca cag ttg ctg Ala Arg Ile Gly Leu Trp Ser Phe Asp Leu Thr Val Thr Gln Leu Leu	465	470	1440
			475
			480
caa gaa aat gta att gaa tct gaa aga ggc att ata aat ggt gta cag Gln Glu Asn Val Ile Glu Ser Glu Arg Gly Ile Ile Asn Gly Val Gln	485	490	1488
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aac tcc atg aac tat ctt ctt gat ctt ctg cat ttc atc atg gtc atc Asn Ser Met Asn Tyr Leu Leu Asp Leu Leu His Phe Ile Met Val Ile	500	505	1536
			510
ctg gct cca aat cct gaa gct ttt ggc ttg ctc gta ttg att tca gtc Leu Ala Pro Asn Pro Glu Ala Phe Gly Leu Leu Val Leu Ile Ser Val	515	520	1584
			525
tcc ttt gtg gca atg ggc cac att atg tat ttc cga ttt gcc caa aat Ser Phe Val Ala Met Gly His Ile Met Tyr Phe Arg Phe Ala Gln Asn	530	535	1632
			540
act ctg gga aac aag ctc ttt gct tgc ggt cct gat gca aaa gaa gtt Thr Leu Gly Asn Lys Leu Phe Ala Cys Gly Pro Asp Ala Lys Glu Val	545	550	1680
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<213> Homo sapiens

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20 25 30

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35 40 45

Phe Leu Val Glu Leu Tyr Gly Asn Ser Leu Leu Leu Thr Ala Val Tyr
50 55 60

Gly Leu Val Val Ala Gly Ser Val Leu Val Leu Gly Ala Ile Ile Gly
65 70 75 80

Asp Trp Val Asp Lys Asn Ala Arg Leu Lys Val Ala Gln Thr Ser Leu
85 90 95

Val Val Gln Asn Val Ser Val Ile Leu Cys Gly Ile Ile Leu Met Met
100 105 110

Val Phe Leu His Lys His Glu Leu Leu Thr Met Tyr His Gly Trp Val
115 120 125

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Leu Ala Ser Thr Ala Thr Ala Ile Thr Ile Gln Arg Asp Trp Ile Val
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Val Val Ala Gly Glu Asp Arg Ser Lys Leu Ala Asn Met Asn Ala Thr
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Ile Arg Arg Ile Asp Gln Leu Thr Asn Ile Leu Ala Pro Met Ala Val
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Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys Gly Phe Ile
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Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val Leu Leu Trp
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Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala Gly Leu Lys
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Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys Asp Ser Asn
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Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala Ser Gln Met
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Ala Glu Pro Phe Arg Thr Phe Arg Asp Gly Trp Val Ser Tyr Tyr Asn
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Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu Tyr Met Thr
305 310 315 320

Val Leu Gly Phe Asp Cys Ile Thr Thr Gly Tyr Ala Tyr Thr Gln Gly
325 330 335

Leu Ser Gly Ser Ile Leu Ser Ile Leu Met Gly Ala Ser Ala Ile Thr
340 345 350

Gly Ile Met Gly Thr Val Ala Phe Thr Trp Leu Arg Arg Lys Cys Gly
355 360 365

Leu Val Arg Thr Gly Leu Ile Ser Gly Leu Ala Gln Leu Ser Cys Leu
370 375 380

Ile Leu Cys Val Ile Ser Val Phe Met Pro Gly Ser Pro Leu Asp Leu
385 390 395 400

Ser Val Ser Pro Phe Glu Asp Ile Arg Ser Arg Phe Ile Gln Gly Glu
405 410 415

Ser Ile Thr Pro Thr Lys Ile Pro Glu Ile Thr Thr Glu Ile Tyr Met
420 425 430

Ser Asn Gly Ser Asn Ser Ala Asn Ile Val Pro Glu Thr Ser Pro Glu
435 440 445

Ser Val Pro Ile Ile Ser Val Ser Leu Leu Phe Ala Gly Val Ile Ala
450 455 460

Ala Arg Ile Gly Leu Trp Ser Phe Asp Leu Thr Val Thr Gln Leu Leu
465 470 475 480

Gln Glu Asn Val Ile Glu Ser Glu Arg Gly Ile Ile Asn Gly Val Gln

485

490

495

Asn Ser Met Asn Tyr Leu Leu Asp Leu Leu His Phe Ile Met Val Ile
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Leu Ala Pro Asn Pro Glu Ala Phe Gly Leu Leu Val Leu Ile Ser Val
 515 520 525

Ser Phe Val Ala Met Gly His Ile Met Tyr Phe Arg Phe Ala Gln Asn
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Arg Lys Glu Asn Gln Ala Asn Thr Ser Val Val
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<221> CDS
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<223> cDNA encoding a ferroportin 1 mutated in position (G80).

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Ser Leu Ser Thr Trp Gly Asp Arg Met Trp His Phe Ala Val Ser Val
35 40 45

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Phe Leu Val Glu Leu Tyr Gly Asn Ser Leu Leu Leu Thr Ala Val Tyr
50 55 60

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Gly Leu Val Val Ala Gly Ser Val Leu Val Leu Gly Ala Ile Ile Ser
65 70 75 80

gac tgg gtg gac aag aat gct aga ctt aaa gtg gcc cag acc tcg ctg 288
Asp Trp Val Asp Lys Asn Ala Arg Leu Lys Val Ala Gln Thr Ser Leu
85 90 95

gtg gta cag aat gtt tca gtc atc ctg tgt gga atc atc ctg atg atg 336
Val Val Gln Asn Val Ser Val Ile Leu Cys Gly Ile Ile Leu Met Met

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ctc act tcc tgc tat atc ctg atc atc act att gca aat att gca aat Leu Thr Ser Cys Tyr Ile Leu Ile Thr Ile Ala Asn Ile Ala Asn 130	135	140	432
ttg gcc agt act gct act gca atc aca atc caa agg gat tgg att gtt Leu Ala Ser Thr Ala Thr Ala Ile Thr Ile Gln Arg Asp Trp Ile Val 145	150	155	480
gtt gtt gca gga gaa gac aga agc aaa cta gca aat atg aat gcc aca Val Val Ala Gly Glu Asp Arg Ser Lys Leu Ala Asn Met Asn Ala Thr 165	170	175	528
ata cga agg att gac cag tta acc aac atc tta gcc ccc atg gct gtt Ile Arg Arg Ile Asp Gln Leu Thr Asn Ile Leu Ala Pro Met Ala Val 180	185	190	576
ggc cag att atg aca ttt ggc tcc cca gtc atc ggc tgt ggc ttt att Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys Gly Phe Ile 195	200	205	624
tcg gga tgg aac ttg gta tcc atg tgc gtg gag tac gtc ctg ctc tgg Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val Leu Leu Trp 210	215	220	672
aag gtt tac cag aaa acc cca gct cta gct gtg aaa gct ggt ctt aaa Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala Gly Leu Lys 225	230	235	720
gaa gag gaa act gaa ttg aaa cag ctg aat tta cac aaa gat act gag Glu Glu Glu Thr Glu Leu Lys Gln Leu Asn Leu His Lys Asp Thr Glu 245	250	255	768
cca aaa ccc ctg gag gga act cat cta atg ggt gtg aaa gac tct aac Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys Asp Ser Asn 260	265	270	816
atc cat gag ctt gaa cat gag caa gag cct act tgt gcc tcc cag atg Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala Ser Gln Met 275	280	285	864
gct gag ccc ttc cgt acc ttc cga gat gga tgg gtc tcc tac tac aac Ala Glu Pro Phe Arg Thr Phe Arg Asp Gly Trp Val Ser Tyr Tyr Asn 290	295	300	912
cag cct gtg ttt ctg gct ggc atg ggt ctt gct ttc ctt tat atg act Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu Tyr Met Thr 305	310	315	960
gtc ctg ggc ttt gac tgc atc acc aca ggg tac gcc tac act cag gga Val Leu Gly Phe Asp Cys Ile Thr Thr Gly Tyr Ala Tyr Thr Gln Gly 325	330	335	1008
ctg agt ggt tcc atc ctc agt att ttg atg gga gca tca gct ata act Leu Ser Gly Ser Ile Leu Ser Ile Leu Met Gly Ala Ser Ala Ile Thr 340	345	350	1056

gga ata atg gga act gta gct ttt act tgg cta cgt cga aaa tgt ggt Gly Ile Met Gly Thr Val Ala Phe Thr Trp Leu Arg Arg Lys Cys Gly	1104
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385 390 395 400	
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405 410 415	
tca att aca cct acc aag ata cct gaa att aca act gaa ata tac atg Ser Ile Thr Pro Thr Lys Ile Pro Glu Ile Thr Thr Glu Ile Tyr Met	1296
420 425 430	
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435 440 445	
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<213> Homo sapiens

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35 40 45

Phe Leu Val Glu Leu Tyr Gly Asn Ser Leu Leu Leu Thr Ala Val Tyr
50 55 60

Gly Leu Val Val Ala Gly Ser Val Leu Val Leu Gly Ala Ile Ile Ser
65 70 75 80

Asp Trp Val Asp Lys Asn Ala Arg Leu Lys Val Ala Gln Thr Ser Leu
85 90 95

Val Val Gln Asn Val Ser Val Ile Leu Cys Gly Ile Ile Leu Met Met
100 105 110

Val Phe Leu His Lys His Glu Leu Leu Thr Met Tyr His Gly Trp Val
115 120 125

Leu Thr Ser Cys Tyr Ile Leu Ile Ile Thr Ile Ala Asn Ile Ala Asn
130 135 140

Leu Ala Ser Thr Ala Thr Ala Ile Thr Ile Gln Arg Asp Trp Ile Val
145 150 155 160

Val Val Ala Gly Glu Asp Arg Ser Lys Leu Ala Asn Met Asn Ala Thr
165 170 175

Ile Arg Arg Ile Asp Gln Leu Thr Asn Ile Leu Ala Pro Met Ala Val
180 185 190

Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys Gly Phe Ile
195 200 205

Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val Leu Leu Trp
210 215 220

Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala Gly Leu Lys

225 230 235 240

Glu Glu Glu Thr Glu Leu Lys Gln Leu Asn Leu His Lys Asp Thr Glu
245 250 255

Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys Asp Ser Asn
260 265 270

Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala Ser Gln Met
275 280 285

Ala Glu Pro Phe Arg Thr Phe Arg Asp Gly Trp Val Ser Tyr Tyr Asn
290 295 300

Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu Tyr Met Thr
305 310 320

Val Leu Gly Phe Asp Cys Ile Thr Thr Gly Tyr Ala Tyr Thr Gln Gly
325 330 335

Leu Ser Gly Ser Ile Leu Ser Ile Leu Met Gly Ala Ser Ala Ile Thr
340 345 350

Gly Ile Met Gly Thr Val Ala Phe Thr Trp Leu Arg Arg Lys Cys Gly
355 360 365

Leu Val Arg Thr Gly Leu Ile Ser Gly Leu Ala Gln Leu Ser Cys Leu
370 375 380

Ile Leu Cys Val Ile Ser Val Phe Met Pro Gly Ser Pro Leu Asp Leu
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Ser Val Ser Pro Phe Glu Asp Ile Arg Ser Arg Phe Ile Gln Gly Glu
405 410 415

Ser Ile Thr Pro Thr Lys Ile Pro Glu Ile Thr Thr Glu Ile Tyr Met
420 425 430

Ser Asn Gly Ser Asn Ser Ala Asn Ile Val Pro Glu Thr Ser Pro Glu
435 440 445

Ser Val Pro Ile Ile Ser Val Ser Leu Leu Phe Ala Gly Val Ile Ala
450 455 460

Ala Arg Ile Gly Leu Trp Ser Phe Asp Leu Thr Val Thr Gln Leu Leu
465 470 475 480

Gln Glu Asn Val Ile Glu Ser Glu Arg Gly Ile Ile Asn Gly Val Gln
485 490 495

Asn Ser Met Asn Tyr Leu Leu Asp Leu Leu His Phe Ile Met Val Ile
500 505 510

Leu Ala Pro Asn Pro Glu Ala Phe Gly Leu Leu Val Leu Ile Ser Val
515 520 525

Ser Phe Val Ala Met Gly His Ile Met Tyr Phe Arg Phe Ala Gln Asn
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Thr Leu Gly Asn Lys Leu Phe Ala Cys Gly Pro Asp Ala Lys Glu Val
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Arg Lys Glu Asn Gln Ala Asn Thr Ser Val Val
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<223> cDNAencoding a ferroportin 1 mutated in position 174 (N174)

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Ser Leu Ser Thr Trp Gly Asp Arg Met Trp His Phe Ala Val Ser Val
35 40 45

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Gly Leu Val Val Ala Gly Ser Val Leu Val Leu Gly Ala Ile Ile Gly
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Asp Trp Val Asp Lys Asn Ala Arg Leu Lys Val Ala Gln Thr Ser Leu
85 90 95

gtg gta cag aat gtt tca gtc atc ctg tgt gga atc atc ctg atg atg		336	
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ctc act tcc tgc tat atc ctg atc atc act att gca aat att gca aat		432	
Leu Thr Ser Cys Tyr Ile Leu Ile Thr Ile Ala Asn Ile Ala Asn			
130	135	140	
ttg gcc agt act gct act gca atc aca atc caa agg gat tgg att gtt		480	
Leu Ala Ser Thr Ala Thr Ala Ile Thr Ile Gln Arg Asp Trp Ile Val			
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gtt gtt gca gga gaa gac aga agc aaa cta gca aat atg att gcc aca		528	
Val Val Ala Gly Glu Asp Arg Ser Lys Leu Ala Asn Met Ile Ala Thr			
165	170	175	
ata cga agg att gac cag tta acc aac atc tta gcc ccc atg gct gtt		576	
Ile Arg Arg Ile Asp Gln Leu Thr Asn Ile Leu Ala Pro Met Ala Val			
180	185	190	
ggc cag att atg aca ttt ggc tcc cca gtc atc ggc tgt ggc ttt att		624	
Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys Gly Phe Ile			
195	200	205	
tcg gga tgg aac ttg gta tcc atg tgc gtg gag tac gtc ctg ctc tgg		672	
Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val Leu Leu Trp			
210	215	220	
aag gtt tac cag aaa acc cca gct cta gct gtg aaa gct ggt ctt aaa		720	
Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala Gly Leu Lys			
225	230	235	240
gaa gag gaa act gaa ttg aaa cag ctg aat tta cac aaa gat act gag		768	
Glu Glu Glu Thr Glu Leu Lys Gln Leu Asn Leu His Lys Asp Thr Glu			
245	250	255	
cca aaa ccc ctg gag gga act cat cta atg ggt gtg aaa gac tct aac		816	
Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys Asp Ser Asn			
260	265	270	
atc cat gag ctt gaa cat gag caa gag cct act tgt gcc tcc cag atg		864	
Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala Ser Gln Met			
275	280	285	
gct gag ccc ttc cgt acc ttc cga gat gga tgg gtc tcc tac tac aac		912	
Ala Glu Pro Phe Arg Thr Phe Arg Asp Gly Trp Val Ser Tyr Tyr Asn			
290	295	300	
cag cct gtg ttt ctg gct ggc atg ggt ctt gct ttc ctt tat atg act		960	
Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu Tyr Met Thr			
305	310	315	320
gtc ctg ggc ttt gac tgc atc acc aca ggg tac gcc tac act cag gga		1008	
Val Lieu Gly Phe Asp Cys Ile Thr Thr Gly Tyr Ala Tyr Thr Gln Gly			
325	330	335	

ctg agt ggt tcc atc ctc agt att ttg atg gga gca tca gct ata act Leu Ser Gly Ser Ile Leu Ser Ile Leu Met Gly Ala Ser Ala Ile Thr 340 345 350	1056
gga ata atg gga act gta gct ttt act tgg cta cgt cga aaa tgt ggt Gly Ile Met Gly Thr Val Ala Phe Thr Trp Leu Arg Arg Lys Cys Gly 355 360 365	1104
ttg gtt cgg aca ggt ctg atc tca gga ttg gca cag ctt tcc tgt ttg Leu Val Arg Thr Gly Leu Ile Ser Gly Leu Ala Gln Leu Ser Cys Leu 370 375 380	1152
atc ttg tgt gtg atc tct gta ttc atg cct gga agc ccc ctg gac ttg Ile Leu Cys Val Ile Ser Val Phe Met Pro Gly Ser Pro Leu Asp Leu 385 390 395 400	1200
tcc gtt tct cct ttt gaa gat atc cga tca agg ttc att caa gga gag Ser Val Ser Pro Phe Glu Asp Ile Arg Ser Arg Phe Ile Gln Gly Glu 405 410 415	1248
tca att aca cct acc aag ata cct gaa att aca act gaa ata tac atg Ser Ile Thr Pro Thr Lys Ile Pro Glu Ile Thr Thr Glu Ile Tyr Met 420 425 430	1296
tct aat ggg tct aat tct gct aat att gtc ccg gag aca agt cct gaa Ser Asn Gly Ser Asn Ser Ala Asn Ile Val Pro Glu Thr Ser Pro Glu 435 440 445	1344
tct gtg ccc ata atc tct gtc agt ctg ctg ttt gca ggc gtc att gct Ser Val Pro Ile Ile Ser Val Ser Leu Leu Phe Ala Gly Val Ile Ala 450 455 460	1392
gct aga atc ggt ctt tgg tcc ttt gat tta act gtg aca cag ttg ctg Ala Arg Ile Gly Leu Trp Ser Phe Asp Leu Thr Val Thr Gln Leu Leu 465 470 475 480	1440
caa gaa aat gta att gaa tct gaa aga ggc att ata aat ggt gta cag Gln Glu Asn Val Ile Glu Ser Glu Arg Gly Ile Ile Asn Gly Val Gln 485 490 495	1488
aac tcc atg aac tat ctt ctt gat ctt ctg cat ttc atc atg gtc atc Asn Ser Met Asn Tyr Leu Leu Asp Leu Leu His Phe Ile Met Val Ile 500 505 510	1536
ctg gct cca aat cct gaa gct ttt ggc ttg ctc gta ttg att tca gtc Leu Ala Pro Asn Pro Glu Ala Phe Gly Leu Leu Val Leu Ile Ser Val 515 520 525	1584
tcc ttt gtg gca atg ggc cac att atg tat ttc cga ttt gcc caa aat Ser Phe Val Ala Met Gly His Ile Met Tyr Phe Arg Phe Ala Gln Asn 530 535 540	1632
act ctg gga aac aag ctc ttt gct tgc ggt cct gat gca aaa gaa gtt Thr Leu Gly Asn Lys Leu Phe Ala Cys Gly Pro Asp Ala Lys Glu Val 545 550 555 560	1680
agg aag gaa aat caa gca aat aca tct gtt gtt tga Arg Lys Glu Asn Gln Ala Asn Thr Ser Val Val 565 570	1716

<210> 6
<211> 571
<212> PRT
<213> Homo sapiens

<400> 6

Met Thr Arg Ala Gly Asp His Asn Arg Gln Arg Gly Cys Cys Gly Ser
1 5 10 15

Leu Ala Asp Tyr Leu Thr Ser Ala Lys Phe Leu Leu Tyr Leu Gly His
20 25 30

Ser Leu Ser Thr Trp Gly Asp Arg Met Trp His Phe Ala Val Ser Val
35 40 45

Phe Leu Val Glu Leu Tyr Gly Asn Ser Leu Leu Leu Thr Ala Val Tyr
50 55 60

Gly Leu Val Val Ala Gly Ser Val Leu Val Leu Gly Ala Ile Ile Gly
65 70 75 80

Asp Trp Val Asp Lys Asn Ala Arg Leu Lys Val Ala Gln Thr Ser Leu
85 90 95

Val Val Gln Asn Val Ser Val Ile Leu Cys Gly Ile Ile Leu Met Met
100 105 110

Val Phe Leu His Lys His Glu Leu Leu Thr Met Tyr His Gly Trp Val
115 120 125

Leu Thr Ser Cys Tyr Ile Leu Ile Ile Thr Ile Ala Asn Ile Ala Asn
130 135 140

Leu Ala Ser Thr Ala Thr Ala Ile Thr Ile Gln Arg Asp Trp Ile Val
145 150 155 160

Val Val Ala Gly Glu Asp Arg Ser Lys Leu Ala Asn Met Ile Ala Thr
165 170 175

Ile Arg Arg Ile Asp Gln Leu Thr Asn Ile Leu Ala Pro Met Ala Val
180 185 190

Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys Gly Phe Ile
195 200 205 220

Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val Leu Leu Trp
210 215 220

Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala Gly Leu Lys
225 230 235 240

Glu Glu Glu Thr Glu Leu Lys Gln Leu Asn Leu His Lys Asp Thr Glu
245 250 255

Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys Asp Ser Asn
260 265 270

Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala Ser Gln Met
275 280 285

Ala Glu Pro Phe Arg Thr Phe Arg Asp Gly Trp Val Ser Tyr Tyr Asn
290 295 300

Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu Tyr Met Thr
305 310 315 320

Val Leu Gly Phe Asp Cys Ile Thr Thr Gly Tyr Ala Tyr Thr Gln Gly
325 330 335

Leu Ser Gly Ser Ile Leu Ser Ile Leu Met Gly Ala Ser Ala Ile Thr
340 345 350

Gly Ile Met Gly Thr Val Ala Phe Thr Trp Leu Arg Arg Lys Cys Gly
355 360 365

Leu Val Arg Thr Gly Leu Ile Ser Gly Leu Ala Gln Leu Ser Cys Leu
370 375 380

Ile Leu Cys Val Ile Ser Val Phe Met Pro Gly Ser Pro Leu Asp Leu
385 390 395 400

Ser Val Ser Pro Phe Glu Asp Ile Arg Ser Arg Phe Ile Gln Gly Glu
405 410 415

Ser Ile Thr Pro Thr Lys Ile Pro Glu Ile Thr Thr Glu Ile Tyr Met
420 425 430

Ser Asn Gly Ser Asn Ser Ala Asn Ile Val Pro Glu Thr Ser Pro Glu
435 440 445

Ser Val Pro Ile Ile Ser Val Ser Leu Leu Phe Ala Gly Val Ile Ala
450 455 460

Ala Arg Ile Gly Leu Trp Ser Phe Asp Leu Thr Val Thr Gln Leu Leu
465 470 475 480

Gln Glu Asn Val Ile Glu Ser Glu Arg Gly Ile Ile Asn Gly Val Gln
485 490 495

Asn Ser Met Asn Tyr Leu Leu Asp Leu Leu His Phe Ile Met Val Ile
500 505 510

Leu Ala Pro Asn Pro Glu Ala Phe Gly Leu Leu Val Leu Ile Ser Val
515 520 525

Ser Phe Val Ala Met Gly His Ile Met Tyr Phe Arg Phe Ala Gln Asn
530 535 540

Thr Leu Gly Asn Lys Leu Phe Ala Cys Gly Pro Asp Ala Lys Glu Val
545 550 555 560

Arg Lys Glu Asn Gln Ala Asn Thr Ser Val Val
565 570

<210> 7
<211> 1716
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1716)
<223> cDNA encoding a ferroportina 1 mutated in position 248 (Q248).

<400> 7
atg acc agg gcg gga gat cac aac cgc cag aga gga tgc tgt gga tcc 48
Met Thr Arg Ala Gly Asp His Asn Arg Gln Arg Gly Cys Cys Gly Ser
1 5 10 15

ttg gcc gac tac ctg acc tct gca aaa ttc ctt ctc tac ctt ggt cat 96
Leu Ala Asp Tyr Leu Thr Ser Ala Lys Phe Leu Leu Tyr Leu Gly His
20 25 30

tct ctc tct act tgg gga gat cgg atg tgg cac ttt gcg gtg tct gtg 144
Ser Leu Ser Thr Trp Gly Asp Arg Met Trp His Phe Ala Val Ser Val
35 40 45

ttt ctg gta gag ctc tat gga aac agc ctc ctt ttg aca gca gtc tac 192
Phe Leu Val Glu Leu Tyr Gly Asn Ser Leu Leu Leu Thr Ala Val Tyr
50 55 60

ggg ctg gtg gtc gca ggg tct gtt ctg gtc ctg gga gcc atc atc ggt 240
Gly Leu Val Val Ala Gly Ser Val Leu Val Leu Gly Ala Ile Ile Gly
65 70 75 80

gac tgg gtg gac aag aat gct aga ctt aaa gtg gcc cag acc tcg ctg Asp Trp Val Asp Lys Asn Ala Arg Leu Lys Val Ala Gln Thr Ser Leu	288
85 90 95	
gtg gta cag aat gtt tca gtc atc ctg tgt gga atc atc ctg atg atg Val Val Gln Asn Val Ser Val Ile Leu Cys Gly Ile Ile Leu Met Met	336
100 105 110	
gtt ttc tta cat aaa cat gag ctt ctg acc atg tac cat gga tgg gtt Val Phe Leu His Lys His Glu Leu Leu Thr Met Tyr His Gly Trp Val	384
115 120 125	
ctc act tcc tgc tat atc ctg atc atc act att gca aat att gca aat Leu Thr Ser Cys Tyr Ile Leu Ile Thr Ile Ala Asn Ile Ala Asn	432
130 135 140	
ttg gcc agt act gct act gca atc aca atc caa agg gat tgg att gtt Leu Ala Ser Thr Ala Thr Ala Ile Thr Ile Gln Arg Asp Trp Ile Val	480
145 150 155 160	
gtt gtt gca gga gaa gac aga agc aaa cta gca aat atg aat gcc aca Val Val Ala Gly Glu Asp Arg Ser Lys Leu Ala Asn Met Asn Ala Thr	528
165 170 175	
ata cga agg att gac cag tta acc aac atc tta gcc ccc atg gct gtt Ile Arg Arg Ile Asp Gln Leu Thr Asn Ile Leu Ala Pro Met Ala Val	576
180 185 190	
ggc cag att atg aca ttt ggc tcc cca gtc atc ggc tgt ggc ttt att Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys Gly Phe Ile	624
195 200 205	
tcg gga tgg aac ttg gta tcc atg tgc gtg gag tac gtc ctg ctc tgg Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val Leu Leu Trp	672
210 215 220	
aag gtt tac cag aaa acc cca gct cta gct gtg aaa gct ggt ctt aaa Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala Gly Leu Lys	720
225 230 235 240	
gaa gag gaa act gaa ttg aaa cat ctg aat tta cac aaa gat act gag Glu Glu Glu Thr Glu Leu Lys His Leu Asn Leu His Lys Asp Thr Glu	768
245 250 255	
cca aaa ccc ctg gag gga act cat cta atg ggt gtg aaa gac tct aac Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys Asp Ser Asn	816
260 265 270	
atc cat gag ctt gaa cat gag caa gag cct act tgt gcc tcc cag atg Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala Ser Gln Met	864
275 280 285	
gct gag ccc ttc cgt acc ttc cga gat gga tgg gtc tcc tac tac aac Ala Glu Pro Phe Arg Thr Phe Arg Asp Gly Trp Val Ser Tyr Tyr Asn	912
290 295 300	
cag cct gtg ttt ctg gct ggc atg ggt ctt gct ttc ctt tat atg act Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu Tyr Met Thr	960
305 310 315 320	
gtc ctg ggc ttt gac tgc atc acc aca ggg tac gcc tac act cag gga	1008

Val	Leu	Gly	Phe	Asp	Cys	Ile	Thr	Thr	Gly	Tyr	Ala	Tyr	Thr	Gln	Gly	
						325			330					335		
ctg	agt	ggt	tcc	atc	ctc	agt	att	ttg	atg	gga	gca	tca	gct	ata	act	1056
Leu	Ser	Gly	Ser	Ile	Leu	Ser	Ile	Leu	Met	Gly	Ala	Ser	Ala	Ile	Thr	
						340			345					350		
gga	ata	atg	gga	act	gta	gct	ttt	act	tgg	cta	cgt	cga	aaa	tgt	ggt	1104
Gly	Ile	Met	Gly	Thr	Val	Ala	Phe	Thr	Trp	Leu	Arg	Arg	Lys	Cys	Gly	
						355			360					365		
ttg	gtt	cgg	aca	ggt	ctg	atc	tca	gga	ttg	gca	cag	ctt	tcc	tgt	ttg	1152
Leu	Val	Arg	Thr	Gly	Leu	Ile	Ser	Gly	Leu	Ala	Gln	Leu	Ser	Cys	Leu	
						370			375					380		
atc	ttg	tgt	gtg	atc	tct	gta	ttc	atg	cct	gga	agc	ccc	ctg	gac	ttg	1200
Ile	Leu	Cys	Val	Ile	Ser	Val	Phe	Met	Pro	Gly	Ser	Pro	Leu	Asp	Leu	
						385			390					395		400
tcc	gtt	tct	cct	ttt	gaa	gat	atc	cga	tca	agg	ttc	att	caa	gga	gag	1248
Ser	Val	Ser	Pro	Phe	Glu	Asp	Ile	Arg	Ser	Arg	Phe	Ile	Gln	Gly	Glu	
						405			410					415		
tca	att	aca	cct	acc	aag	ata	cct	gaa	att	aca	act	gaa	ata	tac	atg	1296
Ser	Ile	Thr	Pro	Thr	Lys	Ile	Pro	Glu	Ile	Thr	Thr	Glu	Ile	Tyr	Met	
						420			425					430		
tct	aat	ggg	tct	aat	tct	gct	aat	att	gtc	ccg	gag	aca	agt	cct	gaa	1344
Ser	Asn	Gly	Ser	Asn	Ser	Ala	Asn	Ile	Val	Pro	Glu	Thr	Ser	Pro	Glu	
						435			440					445		
tct	gtg	ccc	ata	atc	tct	gtc	agt	ctg	ctg	ttt	gca	ggc	gtc	att	gct	1392
Ser	Val	Pro	Ile	Ile	Ser	Val	Ser	Leu	Leu	Phe	Ala	Gly	Val	Ile	Ala	
						450			455					460		
gct	aga	atc	ggt	ctt	tgg	tcc	ttt	gat	tta	act	gtg	aca	cag	ttg	ctg	1440
Ala	Arg	Ile	Gly	Leu	Trp	Ser	Phe	Asp	Leu	Thr	Val	Thr	Gln	Leu	Leu	
						465			470					475		480
caa	gaa	aat	gta	att	gaa	tct	gaa	aga	ggc	att	ata	aat	ggt	gta	cag	1488
Gln	Glu	Asn	Val	Ile	Glu	Ser	Glu	Arg	Gly	Ile	Ile	Asn	Gly	Val	Gln	
						485			490					495		
aac	tcc	atg	aac	tat	ctt	ctt	gat	ctt	ctg	cat	ttc	atc	atg	gtc	atc	1536
Asn	Ser	Met	Asn	Tyr	Leu	Leu	Asp	Leu	Leu	His	Phe	Ile	Met	Val	Ile	
						500			505					510		
ctg	gct	cca	aat	cct	gaa	gct	ttt	ggc	ttg	ctc	gta	ttg	att	tca	gtc	1584
Leu	Ala	Pro	Asn	Pro	Glu	Ala	Phe	Gly	Leu	Leu	Val	Leu	Ile	Ser	Val	
						515			520					525		
tcc	ttt	gtg	gca	atg	ggc	cac	att	atg	tat	ttc	cga	ttt	gcc	caa	aat	1632
Ser	Phe	Val	Ala	Met	Gly	His	Ile	Met	Tyr	Phe	Arg	Phe	Ala	Gln	Asn	
						530			535					540		
act	ctg	gga	aac	aag	ctc	ttt	gct	tgc	ggt	cct	gat	gca	aaa	gaa	gtt	1680
Thr	Leu	Gly	Asn	Lys	Leu	Phe	Ala	Cys	Gly	Pro	Asp	Ala	Lys	Glu	Val	
						545			550					555		560
agg	aag	gaa	aat	caa	gca	aat	aca	tct	gtt	gtt	tga					1716
Arg	Lys	Glu	Asn	Gln	Ala	Asn	Thr	Ser	Val	Val						

565

570

<210> 8
<211> 571
<212> PRT
<213> Homo sapiens

<400> 8

Met Thr Arg Ala Gly Asp His Asn Arg Gln Arg Gly Cys Cys Gly Ser
1 5 10 15

Leu Ala Asp Tyr Leu Thr Ser Ala Lys Phe Leu Leu Tyr Leu Gly His
20 25 30

Ser Leu Ser Thr Trp Gly Asp Arg Met Trp His Phe Ala Val Ser Val
35 40 45

Phe Leu Val Glu Leu Tyr Gly Asn Ser Leu Leu Leu Thr Ala Val Tyr
50 55 60

Gly Leu Val Val Ala Gly Ser Val Leu Val Leu Gly Ala Ile Ile Gly
65 70 75 80

Asp Trp Val Asp Lys Asn Ala Arg Leu Lys Val Ala Gln Thr Ser Leu
85 90 95

Val Val Gln Asn Val Ser Val Ile Leu Cys Gly Ile Ile Leu Met Met
100 105 110

Val Phe Leu His Lys His Glu Leu Leu Thr Met Tyr His Gly Trp Val
115 120 125

Leu Thr Ser Cys Tyr Ile Leu Ile Ile Thr Ile Ala Asn Ile Ala Asn
130 135 140

Leu Ala Ser Thr Ala Thr Ala Ile Thr Ile Gln Arg Asp Trp Ile Val
145 150 155 160

Val Val Ala Gly Glu Asp Arg Ser Lys Leu Ala Asn Met Asn Ala Thr
165 170 175

Ile Arg Arg Ile Asp Gln Leu Thr Asn Ile Leu Ala Pro Met Ala Val
180 185 190

Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys Gly Phe Ile
195 200 205

Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val Leu Leu Trp
210 215 220

Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala Gly Leu Lys
225 230 235 240

Glu Glu Glu Thr Glu Leu Lys His Leu Asn Leu His Lys Asp Thr Glu
245 250 255

Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys Asp Ser Asn
260 265 270

Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala Ser Gln Met
275 280 285

Ala Glu Pro Phe Arg Thr Phe Arg Asp Gly Trp Val Ser Tyr Tyr Asn
290 295 300

Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu Tyr Met Thr
305 310 315 320
 >

Val Leu Gly Phe Asp Cys Ile Thr Thr Gly Tyr Ala Tyr Thr Gln Gly
325 330 335

Leu Ser Gly Ser Ile Leu Ser Ile Leu Met Gly Ala Ser Ala Ile Thr
340 345 350

Gly Ile Met Gly Thr Val Ala Phe Thr Trp Leu Arg Arg Lys Cys Gly
355 360 365

Leu Val Arg Thr Gly Leu Ile Ser Gly Leu Ala Gln Leu Ser Cys Leu
370 375 380

Ile Leu Cys Val Ile Ser Val Phe Met Pro Gly Ser Pro Leu Asp Leu
385 390 395 400

Ser Val Ser Pro Phe Glu Asp Ile Arg Ser Arg Phe Ile Gln Gly Glu
405 410 415

Ser Ile Thr Pro Thr Lys Ile Pro Glu Ile Thr Thr Glu Ile Tyr Met
420 425 430

Ser Asn Gly Ser Asn Ser Ala Asn Ile Val Pro Glu Thr Ser Pro Glu
435 440 445

Ser Val Pro Ile Ile Ser Val Ser Leu Leu Phe Ala Gly Val Ile Ala
450 455 460

Ala Arg Ile Gly Leu Trp Ser Phe Asp Leu Thr Val Thr Gln Leu Leu
465 470 475 480

Gln Glu Asn Val Ile Glu Ser Glu Arg Gly Ile Ile Asn Gly Val Gln
485 490 495

Asn Ser Met Asn Tyr Leu Leu Asp Leu Leu His Phe Ile Met Val Ile
500 505 510

Leu Ala Pro Asn Pro Glu Ala Phe Gly Leu Leu Val Leu Ile Ser Val
515 520 525

Ser Phe Val Ala Met Gly His Ile Met Tyr Phe Arg Phe Ala Gln Asn
530 535 540

Thr Leu Gly Asn Lys Leu Phe Ala Cys Gly Pro Asp Ala Lys Glu Val
545 550 555 560

Arg Lys Glu Asn Gln Ala Asn Thr Ser Val Val
565 570

<210> 9
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> polymerase chain reaction primer
<222> (1)..(20)
<223> 5' PCR primer. Exon 1

<400> 9
ggtgctatct ccagttcctt 20

<210> 10
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(20)
<223> 3' PCR primer. Exon1

<400> 10
gttcacagca gagccacatt 20

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<210> 11
<211> 25
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(25)
<223> 5' PCR primer. Exon 2

<400> 11
cagtcattaa agtgactacc atcgc                                25

<210> 12
<211> 24
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(24)
<223> 3' PCR primer. exon 2

<400> 12
ggcttaatac aactggctag aacg                                24

<210> 13
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(23)
<223> 5' PCR primer. Exon 3

<400> 13
cataatgttag ccaggaagtg ccc                                23

<210> 14
<211> 22
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(22)
<223> 3' PCR primer. Exon 3

<400> 14
tccagaggtg gtgccatcta ag                                22

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<210> 15
<211> 24
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(24)
<223> 5' PCR primer. Exon 4

<400> 15
gagacatttt gatgtaatgt acac

24

<210> 16
<211> 24
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(24)
<223> 3' PCR primer. Exon 4

<400> 16
ctaccagata ttcaattttc tgcc

24

<210> 17
<211> 24
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(24)
<223> 5' PCR primer. Exon 5

<400> 17
ccaccaaaga ctatttaaa ctgc

24

<210> 18
<211> 24
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(24)
<223> 3' PCR primer. Exon 5

<400> 18
tcaccaccga tttaaagtga atcc

24

<210> 19

<211> 23
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(23)
<223> 5' PCR primer. Exon 6 .

<400> 19
gtatttgtta aatggcagt ctc

23

<210> 20
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> 3' PCR primer.Exon 6

<400> 20
ccccactggt aataaaacct g

21

<210> 21
<211> 24
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(24)
<223> 5' PCR primer. Exon 7

<400> 21
ggctttatt tctacatgtc ctcc

24

<210> 22
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(23)
<223> 3' PCR primer. Exon 7

<400> 22
acathtaggg aacatttcag atc

23

<210> 23
<211> 24

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(24)
<223> 5' PCR primer. Exon 8

<400> 23
aaggtaactt aaagacagtc aggc

24

<210> 24
<211> 24
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(24)
<223> 3' PCR primer. Exon 8

<400> 24
gctgacttag gtttcctaaa cagc

24

<210> 25
<211> 10
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(10)
<223> oligonucleotide comprising the polymorphism at nt 238

<400> 25
atcagtgact

10

<210> 26
<211> 10
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> oligonucleotide comprising the polymorphism at nt 521.

<400> 26
gatgattgcc

10

<210> 27
<211> 10
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(10)
<223> oligonucleotide comprising the polymorphism at nt 744

<400> 27
gaaacatctg 10

<210> 28
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> X different from glycine

<400> 28

Ile Ile Xaa Asp Trp
1 5

<210> 29
<211> 5
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> X different form asparagine

<400> 29

Asn Met Xaa Ala Thr
1 5

<210> 30
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> X different from glutamine

<400> 30

Leu Lys Xaa Leu Asn
1 5